## FIGURE 1

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(1) GGC G	CAC H	GAT D	GGG G	15 AAA K	GGA G	CAC H	CCT P	CTC L	30 CAC H	AGA R	AGA R	GAA E	AAG K	45 CGG R
CAA Q	GCA A	AAA K	CAC-	60 <b>AAA</b> K	CAG Q	CGG R	AAA K	CGC R	75 CTC L	AAG K	TCC S	AGC S	TGT C	90 AAG K
AGA R	(32) CAC H		TTA L	105 TAT Y	gtg V	GAC D	TTC F	AGT S	120 GAT D	GTG V	GGG G	TGG W	AAT N	135 GAC D
TGG W	ATC	GTT V	GCA A	150 CCG P	CCG P	GGG G	TAT Y	CAT H	165 GCC A	TTT F	TAC Y	TGC C	CAT H	180 GGG G
GĀG B	TGC C	CCT P	TTT F	195 CCC P	CTG L	GCC A	GAT D	CAC H	210 CTT L	AAC N	TCC S	ACG T	AAT N	225 CAT H
GEC A	ATT I	CTC V	CAA Q	240 ACT T	CTG L	GTC V	AAC N	TCA S	255 GTT V	AAC N	TCT S	AAG K	ATT I	270 CCC P
K	GCA A	TGC C	TGT C	385 GTC V	CCA P	ACA T	gag E		300 AGC S	GCC A	ATC I	TCC S	atg M	315 CTG L
TÃC Y.	CTT L	GAT D	GAG E	330 AAT N	GAG E		gtg V	GTA V	345 TTA L	AAG K	AAC N		CAG O	360 GAC D
375 (129) 397 407 ATG GTT GTC GAG GGT TGT GGG TGT CGT TAGCACAGCA AAATAAAATA														
417 427 437 447 457 TAAATATATA TATATATATA TTAGAAAAAC AGCAAAAAAA TCAAGTTGAC														
467 477 487 497 507 ACTTTAATAT TTCCCAATGA AGACTTTATT TATGGAATGG AATGGAGAAA														
517 527 537 547 557 AAGAAAACA CAGCTATTTT GAAAACTATA TTTATATCTA CCGAAAAGAA														
GTT	567 577 587 GTTGGGAAAA CAAATATTTT AATCAGAGAA TTATT													

FIGURE 2

2/=

GTCGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT AACTTGCGCA CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT CCGAGCCCCA CCGCCCCTCC ACTCCTCGGC CTTGCCCGAC ACTGAGACGC TGTTCCCAGC GTGAAAAGAG AGACTGCGCG GCCGGCACCC GGGAGAAGGA GGAGGCAAAG AAAAGGAACG GACATTCGGT CCTTGCGCCA GGTCCTTTGA CCAGAGTTTT T TCCATGTGGA CGCTCTTTCA ATGGACGTGT CCCCGCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT HJ (1) CGACC ATG GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC MET Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val TCTC CTG GGC GGC GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC GCG Theu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe Ala (24)GCG GCG TCG TCG GGC CCC TCA TCC CAG CCC TCT GAC GAG GTC CTG AGC GAG Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val Leu Ser Glu TTC GAG TTG CGG CTG AGC ATG TTC GGC CTG AAA CAG AGA CCC ACC CCC AGC Phe Glu Leu Arg Leu Leu Ser MET Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser 

AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC CTG TAT CGC AGG CAC TCA GGT Arg Asp Ala Val Val Pro Pro Tyr MET Leu Asp Leu Tyr Arg Arg His Ser Gly

CAG CCG GGC TCA CCC GCC CCA GAC CAC CGG TTG GAG AGG GCA GCC AGC CGA GCC Gln Pro Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg Ala

# FIGURE 2 (CON'T)

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	•		685					700					715				
								GAA					GAA	CTA			
Asn	Thr	Val	Arg	Ser	Phe	His	His	Glu	Glu	Ser	Leu	Glu	Glu	Leu	Pro	Glu	Thr
730					745					760					775		
														ATC			
Ser	GTÅ	гÀг	Thr	THE	Arg	Arg	Pne	Pne	Pne	ASI	Leu	ser	ser	Ile	Pro	Thr	Glu
		790					805					820					835
														ATG MET			
GIU	rne	116	IIIL	SEL	VIG	GIU	Dea	GIII	Val	Lile	Arg	GIU	GIII	PLE I	GIII	изр	AId
നന്	CCA	220	2 2 M	850	3 CM	mma	Cam	C3.C	865	3 000	3.30	3.00	(D 3 /M	880 GAA	3700	3.073	
Leu	Gly	Asn	Asn	Ser	Ser	Phe	His	His	Arg	Ile	Asn	Ile	TVT	GAA	Ile	Ile	AAA Lvs
To the second se													-2-				-1-
CCT	895 GCA	ACA	GCC	AAC	TCG	910 AAA	ጥጥር	CCC	GTG	ACC	925	ርጥጥ	ጥጥር	GAC	A C C	940	መጥር
Pro	Ala	Thr	Ala	Asn	Ser	Lys	Phe	Pro	Val	Thr	Arg	Leu	Leu	Asp	Thr	Arg	Leu
age design			955					970					005			_	
GTG	AAT	CAG		GCA	AGC	AGG	TGG		AGT	TTT	GAT	GTC	985 ACC	ccc	GCT	GTG	ATG
Val	Asn	Gln	Asn	Ala	Ser	Arg	Trp	Glu	Ser	Phe	Asp	Val	Thr	Pro	Ala	Val	MET
1000	כ				1015				1	L030				1	.045		
CGG	TGG	ACT	GCA	CAG	GGA	CAC	GCC	AAC	CAT	GGA	TTC	GTG	GTG	GAA	GTG	GCC	CAC
Arg	urp	Thr	Ala	Gln	GLY	His	Ala	Asn	His	Gly	Phe	Val	Val	Glu	Val	Ala	His
Continue Spannings Co. C. Standards		1060					L075			1	]	1090				3	105
TTG Leu	GAG	GAG	AAA	CAA	GGT	GTC	TCC	AAG	AGA	CAT	GTT	AGG	ATA	AGC	AGG	TCT	TTG
		914	цуа	GIH	GLY	AGT	Set	гу	Arg	nis	vaı	Arg		ser (247)		Ser	Leu
*			,	1120										. ,			
CAC	CAA	GAT			AGC	TGG	TCA	CAG	L135 ATA	AGG	CCA	ጥጥር	CTA	L150 GTA	<b>አ</b> ርጥ	ம்ப்பு	GGC
His	Gln	Asp	Glu	His	Ser	Trp	Ser	Gln	Ile	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly
														(	(266)	•	_
	1165				ב	180				]	195				נ	210	
CAT	GAT	GGA	AAA	GGG	CAT	CCT	CTC	CAC	AAA	AGA	GAA	AAA	CGT	CAA	GCC	ΔΔΔ	CAC
1772	wsb	GTA	rĀs	GIY	HIS	Pro	Leu	His	Lys	Arg	Glu	Lys		Gln (283)		Lys	His
		_											,	(203)			
AAA	CAG		L225 AAA	CGC	Сфф	ΔAG	<b>ጥ</b> ርር	1240 AGC	முகும்	አአሮ	7.07	(299)	1255	TTG	m z c	<b>c</b> mc	<b>63.6</b>
Lys	Gln	Arg	Lys	Arg	Leu	Lys	Ser	Ser	Cys	Lys	Arg	His	Pro	Leu	TVr	Val	Asp
				_		_			-	<b>-</b>					-1-		E
1270					285				13	300				ין:	15		
TTC	AGT	GAC	GTG	GGG	TGG	AAT	GAC	TGG	ATT	GTG	GCT	ccc	CCG	GGG	ጥልጥ	CAC	GCC
File	ser	ASP	val	GIA	Trp	Asn	Asp	Trp	Ile	Va1	Ala	Pro	Pro	Gly	Tyr	His	Ala

# FIGURE 2 (CON'T)

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1330 1345 1360 1375 TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC TCC ACT Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr 1390 1405 1420 AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT AAG ATT CCT AAG Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys 1435 1450 1465 GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG ATG CTG TAC CTT GAC GAG Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser MET Leu Tyr Leu Asp Glu 1495 1510 1525 AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG GAC ATG GTT GTG GAG GGT TGT GGG Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp MET Val Val Glu Gly Cys Gly 1540(396) 1553 1563 1573 1583 1593 TGT CGC TAGTACAGCA AAATTAAATA CATAAATATA TATATATA TATATTTTAG AAAAAAGAAA Cys Arg

AAAA

#### FIGURE 3

CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCCC GGAGCCCGGC CCGGAAGCTA GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG AGTATCTAGC TTGTCTCCCC GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC ACAGTCCCCG GCCCTCGCCC AGGTTCACTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG LEG (1) CTGTCAAGAA TCATGGACTG TTATTATATG CCTTGTTTTC TGTCAAGACA CC ATG ATT CCT MET Ile Pro ũ GGT AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC GCG Gly Asn Arg MET Leu MET Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly Ala AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC GAG ATT CAG Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Val Ala Glu Ile Gln GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG CTC CTG CGG GAC TTC Gly His Ala Gly Gly Arg Arg Ser Gly Gln Ser His Glu Leu Leu Arg Asp Phe GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC CGC CCG CAG CCT AGC AAG Glu Ala Thr Leu Leu Gln MET Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys

AGT GCC GTC ATT CCG GAC TAC ATG CGG GAT CTT TAC CGG CTT CAG TCT GGG GAG Ser Ala Val Ile Pro Asp Tyr MET Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu

5-1

### FIGURE 3 (CON'T)

687 702 717 GAG GAG GAA GAG CAG ATC CAC AGC ACT GGT CTT GAG TAT CCT GAG CGC CCG GCC Glu Glu Glu Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala 747 762 AGC CGG GCC AAC ACC GTG AGG AGC TTC CAC CAC GAA GAA CAT CTG GAG AAC ATC. Ser Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn Ile 807 822 CCA GGG ACC AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu Ser Ser Ile 867 882 CCT GAG AAC GAG GTG ATC TCC TCT GCA GAG CTT CGG CTC TTC CGG GAG CAG GTG Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu Phe Arg Glu Gln Val 912 927 GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT TAT GAG GTT Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile Tyr Glu Val 957 972 987 ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC ACA CGA CTA CTG GAC MET Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile Thr Arg Leu Leu Asp 1017 1032 ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG GAA ACT TTT GAT GTG AGC CCT Thr Arg Leu Val His His Asn Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro 1062 1077 1092 GCG GTC CTT CGC TGG ACC CGG GAG AAG CAG CCA AAC TAT GGG CTA GCC ATT GAG Ala Val Leu Arg Trp Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu 1137 GTG ACT CAC CTC CAT CAG ACT CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC 1167 Val Thr His Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser 1182 1197 1212 CGA TCG TTA CCT CAA GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC Arg Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val 1227 1242 1257 ACC TTT GGC CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg Ala Lys 1302 1317 CGT AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC CGG Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys Arg (293)

### FIGURE 3 (CON'T)

1332(311) 1347 1362 1377
CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC TGG ATT GTG
Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val

1392 1407 1422 1437
GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC TGC CCC TTT CCA CTG
Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp Cys Pro Phe Pro Leu

1452 1467 1482
GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT GTG CAG ACC CTG GTC AAT TCT
Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser

1497 1512 1527 1542
GTC AAT TCC AGT ATC CCC AAA GCC TGT TGT GTG CCC ACT GAA CTG AGT GCC ATC
Wal Asn Ser Ser Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile

1557 1572 1587
TCC ATG CTG TAC CTG GAT GAG TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG
Ser MET Leu Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys <u>Asn Tyr Gln Glu</u>

1602 1617 (408) 1636 1646 1656 ATG GTA GTA GAG GGA TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG MET Val Val Glu Gly Cys Gly Cys Arg

1666 1676 1686 1696 1706 1716 1726
ATATACACAC CACACACA CACCACACACA CACGTTCCCA TCCACTCACC CACACACTAC

1736 1746 1756 1766 1776 1786 1796 ACAGACTGCT TCCTTATAGC TGGACTTTTA TTTAAAAAAA AAAAAAAAA AATGGAAAAA ATCCCTAAAC

1806 1816 1826 1836 1846 1856 1866 ATTCACCTTG ACCTTATTTA TGACTTTACG TGCAAATGTT TTGACCATAT TGATCATATA TTTTGACAAA

1876 1886 1896 1906 1916 1926 1936 ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG AGTCATTATT TTAAAAAAAA AAAAAAAACT

1946 CTAGAGTCGA CGGAATTC

II.